

FIGURE 1

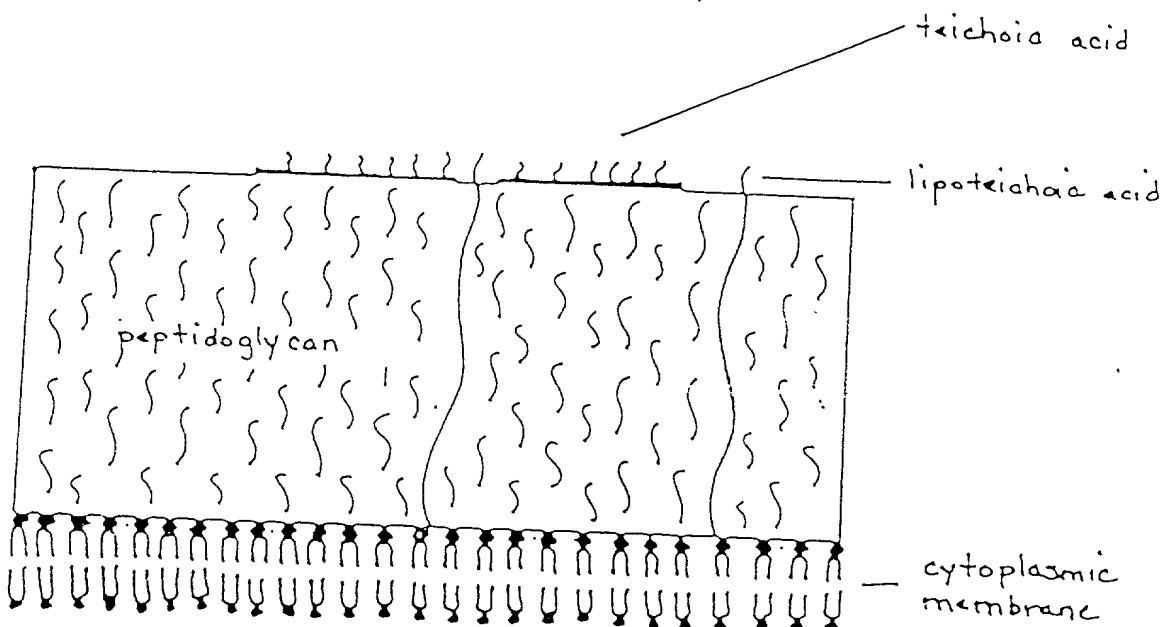


FIGURE 2

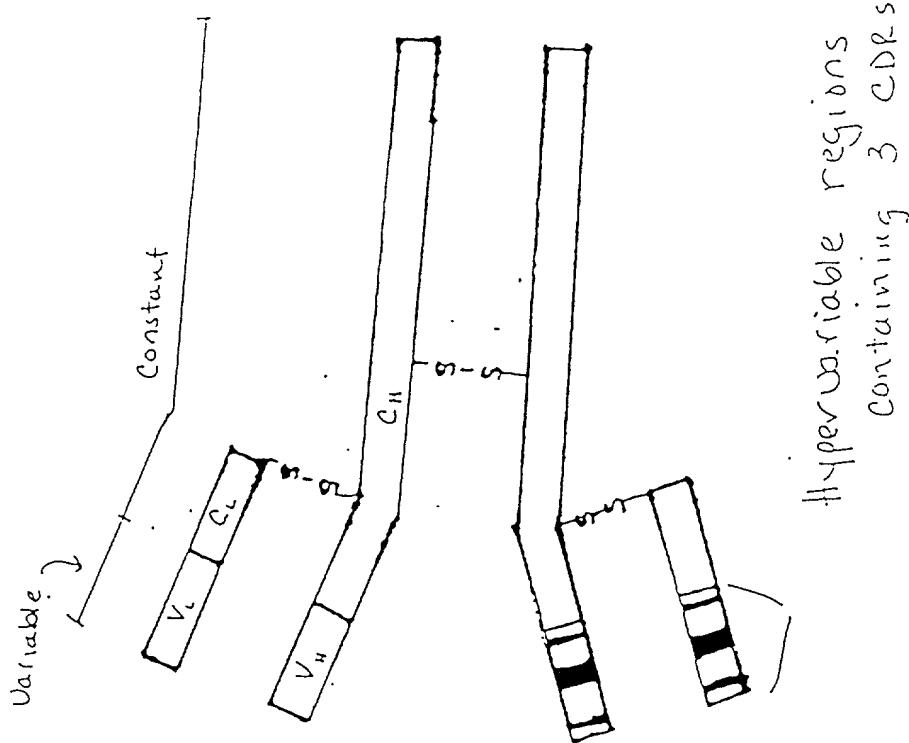
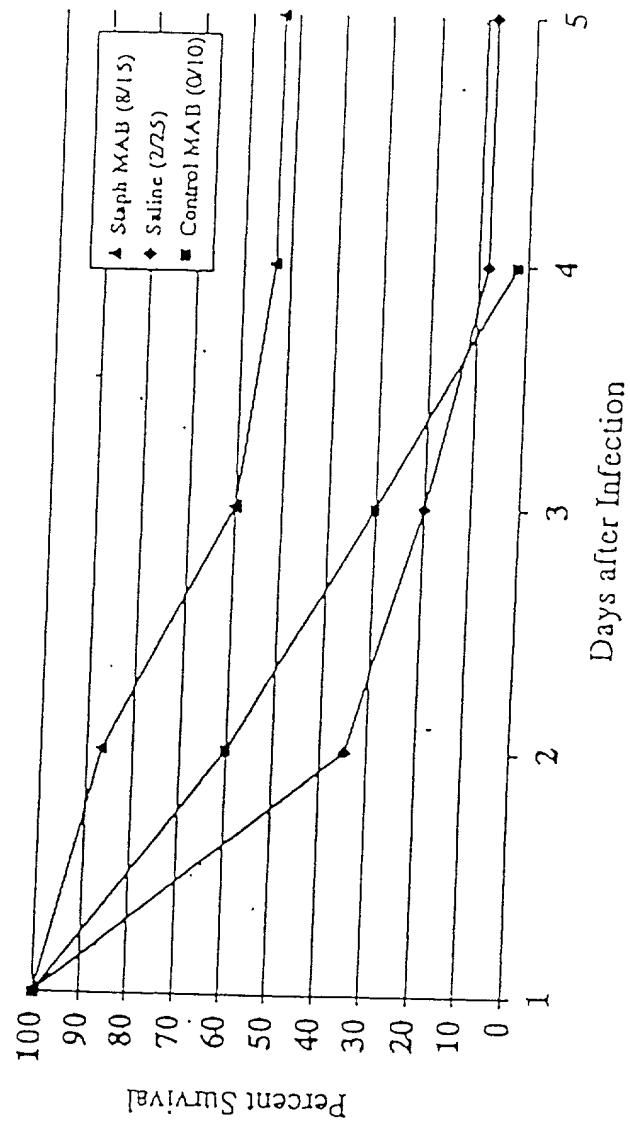


FIGURE 3

Effect of Anti-Staph MAB 96-110 on
Survival in a Lethal *S. aureus* Sepsis Model



Y D S E E D C M S Y E E D C M S

FIGURE 4

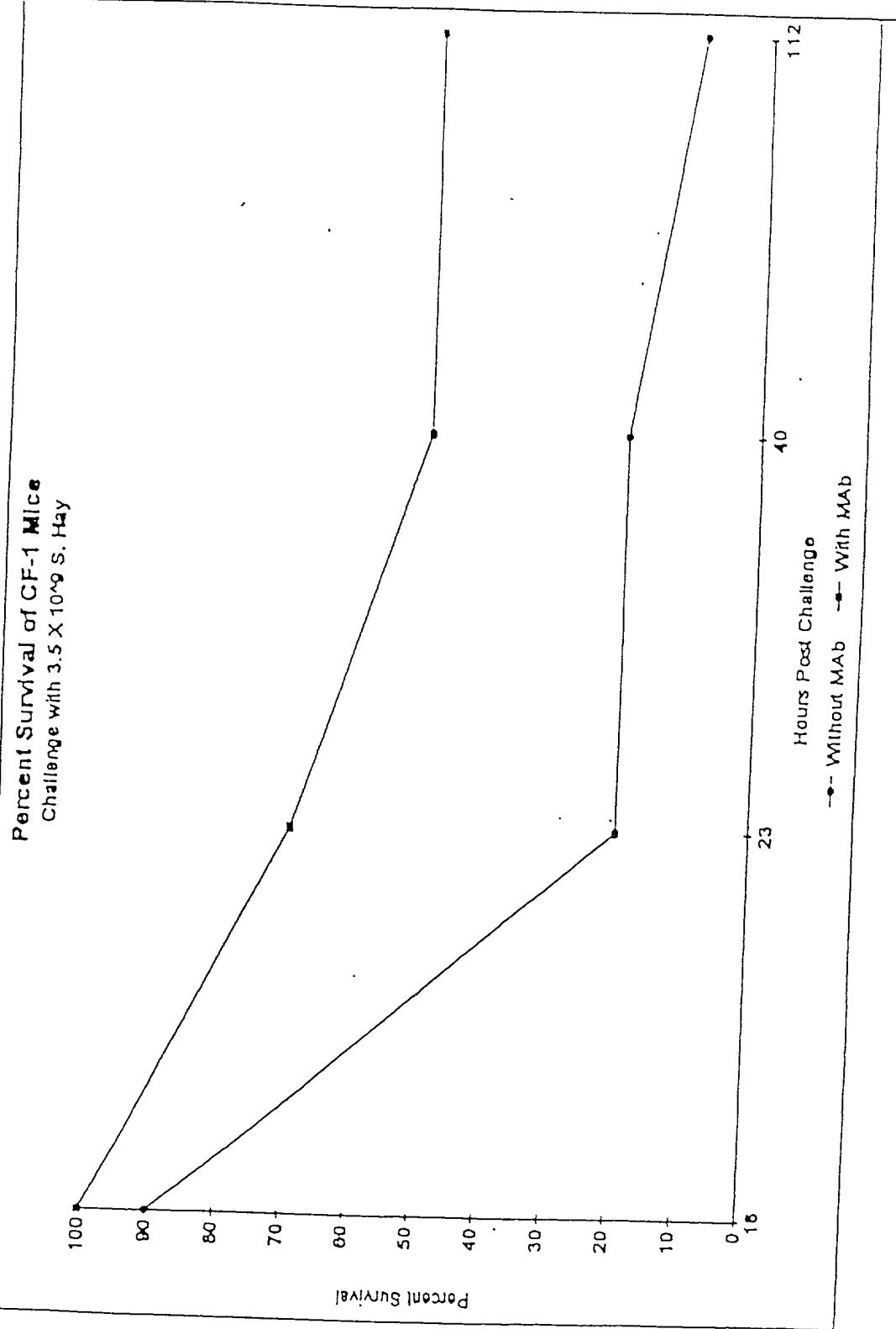


FIGURE 5

6MER. SEQ	10	20	30
1{ 13.6mer2-1	GGGGCTCATC	CGGATAGGCT	TTATGGGGCC
61	C A H A D R V	Y G A	SEQ ID NO 4
12{ 14.6mer2-2	GGGGCTCATC	CGGATAGGCT	TTATGGGGCC
65	G A H A D R V	Y C A	SEQ ID NO.5
13{ 15.6mer2-3	GGGGCTCATC	CGGATACCGCT	TTATGGGGCC
66	G A H A D R V	Y G A	
14{ 16.6mer2-4	CCGA-TCA'IC	CGGATAGGCT	TTATGGGGCC
62	G ? H A D R V	Y C A	SEQ ID NO.6
15{ 17.6mer2-5	GGGGCTCATC	CGGATAGGCT	TTATGGGGCC
67	G A H A D R V	Y G A	SEQ ID NO.7
16{ 18.6mer2-6	GGGGCTCATC	CGGATAGGCT	TTATGGGGCC
68	G A H A D R V	Y G A	
17{ 19.6mer2-7	GGGGCTCATC	CGGATACCGCT	TTATGGGGCC
69	G A H A D R V	Y G A	
18{ 20.6mer2-8	CCCCCTCATC	CGGATAGGCT	TTATGGGGCC
70	G A H A D R V	Y C A	
19{ 21.6mer2-9	GGGGCTCATC	CGGATACCGCT	TTATGGGGCC
71	G A H A D R V	Y G A	
21{ 23.6mer2-11	GGGGCTCATC	CGGATAGGCT	TTATGGGGCC
72	G A H A D R V	Y C A	
22{ 24.6mer2-11	GGGGCTCATC	CGGATACCGCT	TTATGGGGCC
73	G A H A D R V	Y G A	
23{ 25.6mer2-11	CCCCCTCATC	CGGATAGGCT	TTATGGGGCC
74	G A H A D R V	Y - G A	
24{ 26.6mer2-11	CCCCCTCATC	CGGATACCGCT	TTATGGGGCC
75	G A H A D R V	Y G A	
25{ 27.6mer2-15	GGGGCTCATC	CGGATAGGCT	TTATGGGGCC
76	G A H A D R V	Y G A	
26{ 28.6mer2-16	GGGGCTCATC	CGGATAGGCT	TTATGGGGCC
77	G A H A D R V	Y G A	
28{ 30.6mer2-18	GGGGCTCATC	CGGATAGGCT	TTA'ICGGGCC
78	G A H A D R V	Y G A	
29{ 31.6mer2-19	GGGGCTCATC	CGGATAGGCT	TTATGGGGCC
79	G A H A D R V	Y G A	
30{ 32.6mer2-20	GGGGCTCATC	CGGATAGGCT	TTATGGGGCC
80	G A H A D R V	Y G A	

FIGURE 6

15MER2. SEQ		10	20	30	40	50	60
50: 07. 15mer2-1/0	GGGGCTTGGC	ATTCGGCTCA	TCGTATTCTCT	CTTCAGCTTG	CTGCTGGTCG	TGGGCC	SEQ ID NO. 8
70	C A (W)	H W R H R I P	L Q L A A G R	I C A	SEQ ID NO. 9		
52: 09. 15mer2-3/0	GGGGCTTGGC	GGCATGCTAA	TTTTTCTCAT	TTTTTCTCATC	GGTCCTTCAT	TGGGCC	SEQ ID NO. 10
72	G A R (R)	H G N (F)	S (H)	F F H R	S L I C A	SEQ ID NO. 11	
53: 10. 15mer2-4/0	GGGGCTTGGC	AGGCTTTCTT	TAGTCATTCT	TATGCTCC	TCGGTTGGC	TGGGCC	SEQ ID NO. 12
73	G A (W)	K A L (F)	S (H)	S Y R P	R G S A G A	SEQ ID NO. 13	
54: 11. 15mer2-5/0	GGGGCTTGGC	ATTCGGCTCA	TCGTATTCTCT	CTTCAGCTTG	CTGCTGGTCG	TGGGCC	SEQ ID NO. 14
74	G A R	H W R H R I P	L O L A A G R	I C A	SEQ ID NO. 15		
56: 13. 15mer2-7/0	GGGGCTTGGC	ATTCGGCTCA	TCGTATTCTCT	CTTCAGCTTG	CTTCCTGGTCG	TGGGCC	SEQ ID NO. 16
76	G A W	H W R H R I P	L O L A A G R	I C A	SEQ ID NO. 17		
57: 14. 15mer2-8/0	GGGGCTTGGC	ATTCGGCTCA	TCGTATTCTCT	CTTCAGCTTG	CTTCCTGGTCG	TGGGCC	SEQ ID NO. 18
77	G A W	H W R H R I P	L O L A A G R	I C A	SEQ ID NO. 19		
58: 15. 15mer2-9/0	GGGGCTTGGC	TCGGCTGTCTT	CTATCTCTCT	TTGCTCTCATG	CTACTGAGCT	TGGGCC	SEQ ID NO. 20
78	G A Q	V A V L Y P P L	A D A T E L	G A	SEQ ID NO. 21		
59: 16. 15mer2-10/0	GGGGCTTGGC	GGCATGCTAA	TTTTTCTCAT	TTTTTCTCATC	GGTCGTTGAT	TGGGCC	SEQ ID NO. 22
79	G A R	R H G N F S H	F F H R	S L I G A	SEQ ID NO. 23		
60: 17. 15mer2-11/0	GGGGCTTGGC	GGCATGCTAA	TTTTTCTCAT	TTTTTCTCATC	GGTCGTTGAT	TGGGCC	SEQ ID NO. 24
80	G A R	R H G N F S H	F F H R	S L I G A	SEQ ID NO. 25		
61: 18. 15mer2-12/0	GGGGCTTGGC	GTATCTATTT	TTCTCATCT	CATGCCATC	TTCTAGTCC	TGGGCC	SEQ ID NO. 26
81	G A (W)	R H Y (P)	(S) (H)	R H A (H)	L R S P G A	SEQ ID NO. 27	
62: 19. 15mer2-13/0	GGGGCTTGGC	GTATCTATTT	TTCTCATCT	CATGCCATC	TTCTAGTCC	TGGGCC	SEQ ID NO. 28
82	G A W	R H Y F S H R	H A H L R S P	G A	SEQ ID NO. 29		
63: 20. 15mer2-14/0	GGGGCTTGGC	GGAAAGTATT	TTCTTATCAT	CATGCCATC	TTCTAGTCC	TGGGCC	SEQ ID NO. 30
83	G A W	R K Y F S Y H	H A H L C S P	G A	SEQ ID NO. 31		
54: 21. 15mer2-15/0	GGGGCTTGGC	GTATCTATTT	TTCTCATCT	CATGCCATC	TTCTAGTCC	TGGGCC	SEQ ID NO. 32
84	G A W	R M Y F S H R	H A H L R S P	G A	SEQ ID NO. 33		
55: 22. 15mer2-16/0	GGGGCTTGGC	GTATCTATTT	TTCTCATCT	CATGCCATC	TTCTAGTCC	TGGGCC	SEQ ID NO. 34
85	G A W	R M Y F S H R	H A H L R S P	G A	SEQ ID NO. 35		
56: 23. 15mer2-17/0	GGGGCTTGGC	GTATCTATTT	TTCTCATCT	CATGCCATC	TTCTAGTCC	TGGGCC	SEQ ID NO. 36
86	G A W	R M Y F S H R	H A H L R S P	G A	SEQ ID NO. 37		
57: 24. 15mer2-18/0	GGGGCTTGGC	GGCATGCTAA	TTTTTCTCAT	TTTTTCTCATC	GGTCGTTGAT	TGGGCC	SEQ ID NO. 38
87	G A R	R H G N F S H	F F H R S L I	G A	SEQ ID NO. 39		
58: 25. 15mer2-19/0	GGGGCTTGGC	ATTCGGCTCA	TCGTATTCTCT	CTTCAGCTTG	CTGCTGGTCG	TGGGCC	SEQ ID NO. 40
88	G A W	H W R H R I P	L Q L A A G R	I C A	SEQ ID NO. 41		
59: 26. 15mer2-20/0	GGGGCTTGGC	GGCATGCTAA	TTTTTCTCAT	TTTTTCTCATC	GGTCGTTGAT	TGGGCC	SEQ ID NO. 42
89	G A R	R H G N F S H	F F H R S L I	G A	SEQ ID NO. 43		

FIGURE 7

SMER1_SEQ		10	20	30	40	50	60
11	28.15mer1-3/	GGGGCTGGATT	CGATTACCTT	GGATCTCTCT	CATCATGATC	CTCTTCTTTC	TCCCCCCC
12		C A D	W I T F	H R R	H H D	R V L S	G A
13	29.15mer1-3/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
14		G A G	W I T F	H R R	H H D	R V L S	G A
15	32.15mer1-6/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
16		G A G	W I T F	H R R	H H D	R V L S	G A
17	13.15mer1-7/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
18		G A G	W I T F	H R R	H H D	R V L S	G A
19	14.15mer1-8/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
20		G A G	W I T F	H R R	H H D	R V L S	G A
21	15.15mer1-9/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
22		G A G	W I T F	H R R	H H D	R V L S	G A
23	16.15mer1-10/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
24		G A G	W I T F	H R R	H H D	R V L S	G A
25	17.15mer1-11/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
26		G A G	W I T F	H R R	H H D	R V L S	G A
27	18.15mer1-12/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
28		G A C	W I T F	H R R	H H D	R V L S	G A
29	19.15mer1-13/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
30		G A C	W I T F	H R R	H H D	R V L S	G A
31	20.15mer1-14/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
32		G A G	W I T F	H R R	H H D	R V L S	G A
33	21.15mer1-15/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
34		G A G	W I T F	H R R	H H D	R V L S	G A
35	22.15mer1-16/	GGGGCTCGGA	AGGCTATGTT	TATCGATCT	TATCGTCATC	GGGGCTTCGGCC	TGGGGCC
36		G A G	K A M F	S Y H	S Y R H	R G S A	G A
37	23.15mer1-17/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
38		G A C	W I T F	H R R	H H D	R V L S	G A
39	24.15mer1-18/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
40		G A G	W I T F	H R R	H H D	R V L S	G A
41	25.15mer1-19/	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
42		G A G	W I T F	H R R	H H D	R V L S	G A
43	26.15mer1-20/	GGGGCTCGGT	GGATTACTTT	TCATCGTCGT	CATCATGATC	CTCTTCTTTC	TGGGGCC
44		G A G	W I T F	H R R	H H D	R V L S	G A

FIGURE 8

masterlist	10	20	30	40	50	60	70
5' 15mer 1st.1	CGGGCTGATT CGGATTAATT TCACTGCTCT CATCATCTC CTCCTTC TC	CCGCC	CC	CC	CC	CC	CC
57	G A O W L T F K R R H H D R V L S C A	16/17SEQ	ID	No	50		
90 15mer 1st.2	CGGGCTGATT GTCATATCCT TCACTGCTCT CATCATCTC CTCCTTC TC	CCGCC	CC	CC	CC	CC	CC
91	G A S R H M L A R W S R L L A V P G A	1/10	SEQ	ID	No	51	
71' 15mer 1st.16	CGGGCTGATT AGGCTATGTT TACTCATCTT TATCTCATCTC GGGCTTC	CCGCC	CC	CC	CC	CC	CC
85	G A K K A M F S H S Y R H R G S A C A	1/10	SEQ	ID	No	53	
92 15mer 2nd.1	CGGGCTGATT ATTGGCCGCA TGGTATTCCT CTTCATCTC CTCCTTC TC	CCGCC	CC	CC	CC	CC	CC
98	G A H H W R X R I P L Q A A G R G A	1/17	SEQ	ID	No	54	
93 15mer 2nd.3	CGGGCTGTC CGGATCGTAA TTTTTCAT TTTTTCAT GCTCGTGTAT	TC	CC	CC	CC	CC	CC
99	G A R R H G N F S H F F H R S L I G A	1/18	SEQ	ID	No	55	
94 15mer 2nd.4	CGGGCTGGA AGCCCTTCTGGA TGGTATTCCT TATCTCATCTC GGGCTTC	CC	CC	CC	CC	CC	CC
100	G A W X A L F S H S Y R P R C S A C A	1/18	SEQ	ID	No	56	
95 15mer 2nd.9	CGGGCTGAGC TCCCTGTTT CTATCTCTC TGGCTGATC CTACTCAT	TC	CC	CC	CC	CC	CC
101	G A O V A V L Y P P L A D A T E L C A	1/18	SEQ	ID	No	57	
96 15mer 2nd.12	CGGGCTGAGC CTATCTATT TCTCTATGT CTGACCCATC TCCCTAGTC	TC	CC	CC	CC	CC	CC
102	G A W R M Y F S H R H A N L R S P G A	1/18	SEQ	ID	No	58	
97 6mer 2nd.1	CGGGCTGAGC CGGATAGGT TATCCGGCC G A H A D R V Y G A	1/18	SEQ	ID	No	59	
103	CGGGCTGAGC CGGATAGGT TATCCGGCC G A H A D R V Y G A	1/18	SEQ	ID	No	60	

FIGURE 9

Comparison of Signals at 6.25×10^9 vir/mL.

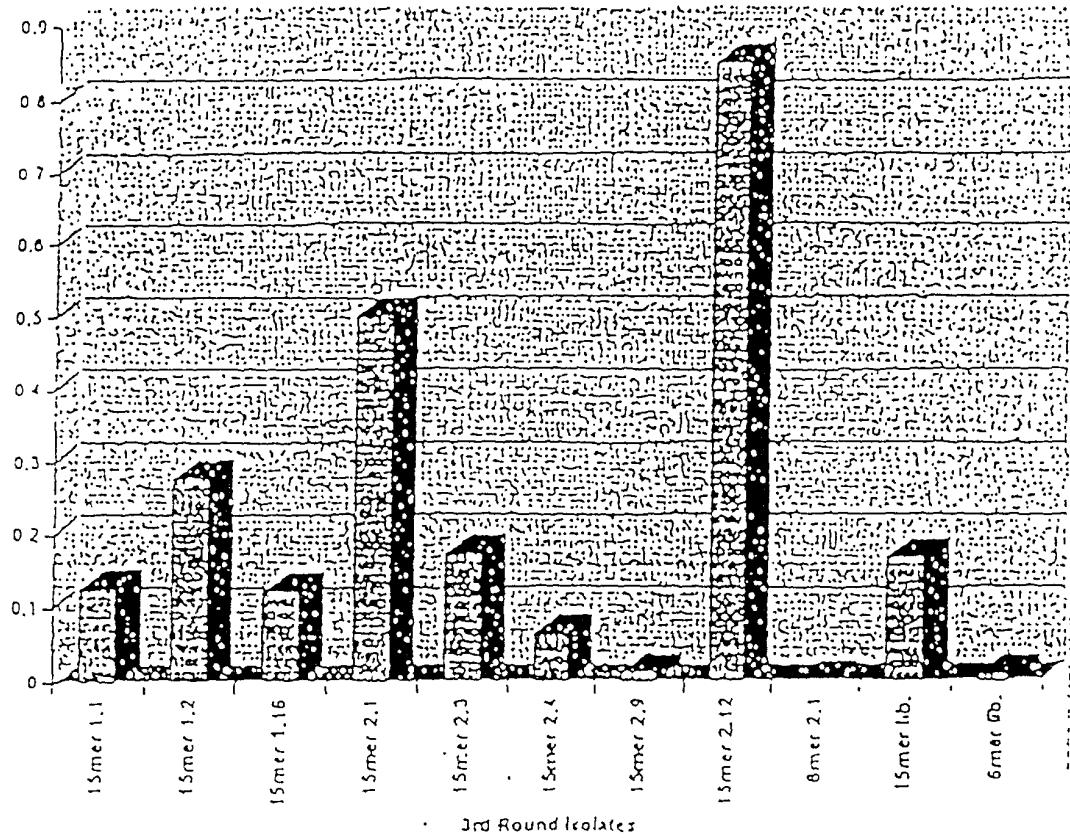


FIGURE 10: General Cloning Strategy

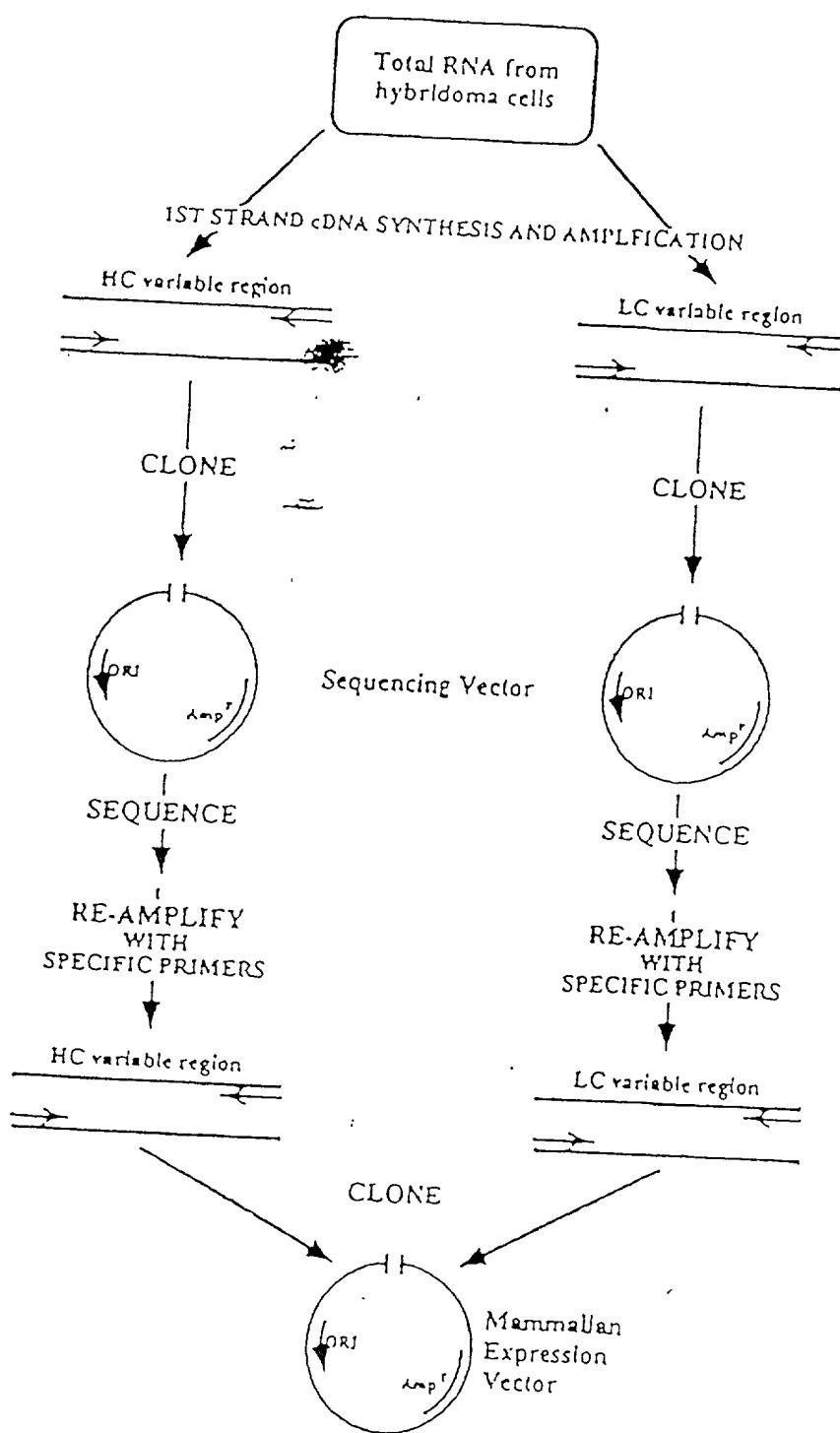


FIGURE 11

Mouse Heavy Chain "front" primers

JSS1
5'-ATTCAGGGCCCAGCCGGCCATGGCCGARGTRMAGCTSAKGAGWC-3' SEQ ID NO 68
JSS2
5'-ATTCAGGGCCCAGCCGGCCATGGCCGARGTYCARCTKCARCARYC-3' SEQ ID NO 69
JSS3
5'-ATTCAGGGCCCAGCCGGCCATGGCCCAGGTGAAGCTKSTSGARTC-3' SEQ ID NO 70
JSS4
5'-ATTCAGGGCCCAGCCGGCCATGGCCGAVGTGMWGCTKGTGGAGWC-3' SEQ ID NO 71
JSS8
5'-ATTCAGGGCCCAGCCGGCCATGGCCAGGTBCARCTRMARSARTC-3' SEQ ID NO 72

Mouse Heavy chain "back" primers

JS160
5'-GCTGCCACCGCCACCTGMRGAGACDGTGASTGARG-3' SEQ ID NO 73
JS161
5'-GCTGCCACCGCCACCTGMRGAGACDGTQASMGTG-3' SEQ ID NO 74
JS162
5'-GCTGCCACCGCCACCTGMRGAGACDGTGASCAGRG-3' SEQ ID NO 75

Mouse Light Chain Leader "front" primers

PMC12
5'-CCCGGGCCACCATGGAGACAGACACACTCCTG-3' SEQ ID NO 76
PMC13
5'-CCCGGGCCACCATGGATTTCAAGTCCAGATTTC-3' SEQ ID NO 77
PMC14
5'-CCCGGGCCACCATGGAGWCACARWCTCAGGTC-3' SEQ ID NO 78
PMC15
5'-CCCGGGCCACCATGKCCCCWRCTCAGYTTCTKG-3' SEQ ID NO 79
PMC55
5'-CCCGGGCACCATGAAGTTGCCTGTTAGGCTG-3' SEQ ID NO 80

Mouse Light Chain "back" primer

OKA57
5'-GCACCTCCAGATGTTAACTGCTC-3' SEQ ID NO 81

"96-110" Specific Primers

96110HF2
5'-TAATATCGCGACAGCTACAGGTGTCCACTCCGAAAGTGATGCTGGAGWCCTG-3' SEQ ID NO 82
96110HB
5'-TTATAQAAATQGTGAGGAGACGGTGAGTGAG-3' SEQ ID NO 83
96110BLF
5'-TTAGGCQATATQGTTCTCTCCAGTCTCC-3' SEQ ID NO 84
96110BLL
5'-GTAACCGTTCQAAAAGTGTACTTACGTTATTCCAGCATGGTCC-3' SEQ ID NO 85

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FIGURE 12

R P T I S R D S Q R S R L Y L Q R N N L K T R D T A R Y Y C
R G A S G I D Y A R D Y H G Q G T S L T V S S S Q Q I D N O 94
S-110 anti-staph (HAY) light chain

Region (type VI)

Q I V L S O S P A I L S A S P G R K V T H T C SEQ ID NO. 96
ΔGGGCACCTGAGTGTAAATTATCATCCAC SEQ ID NO. 98
 R A S S S V N Y H R SEQ. ID NO. 99

CDR Regions Under Consideration

FIGURE 13

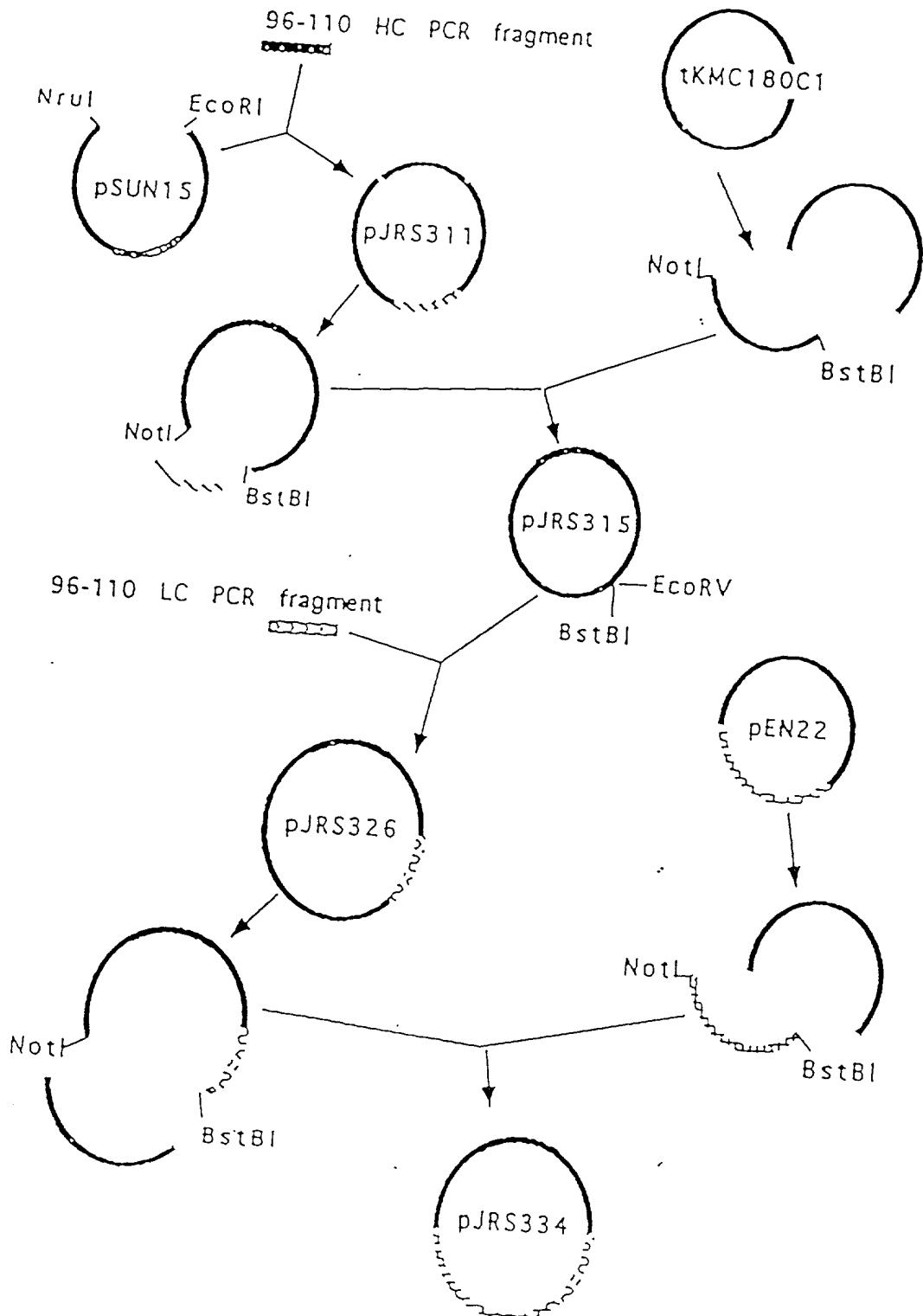


FIGURE 14

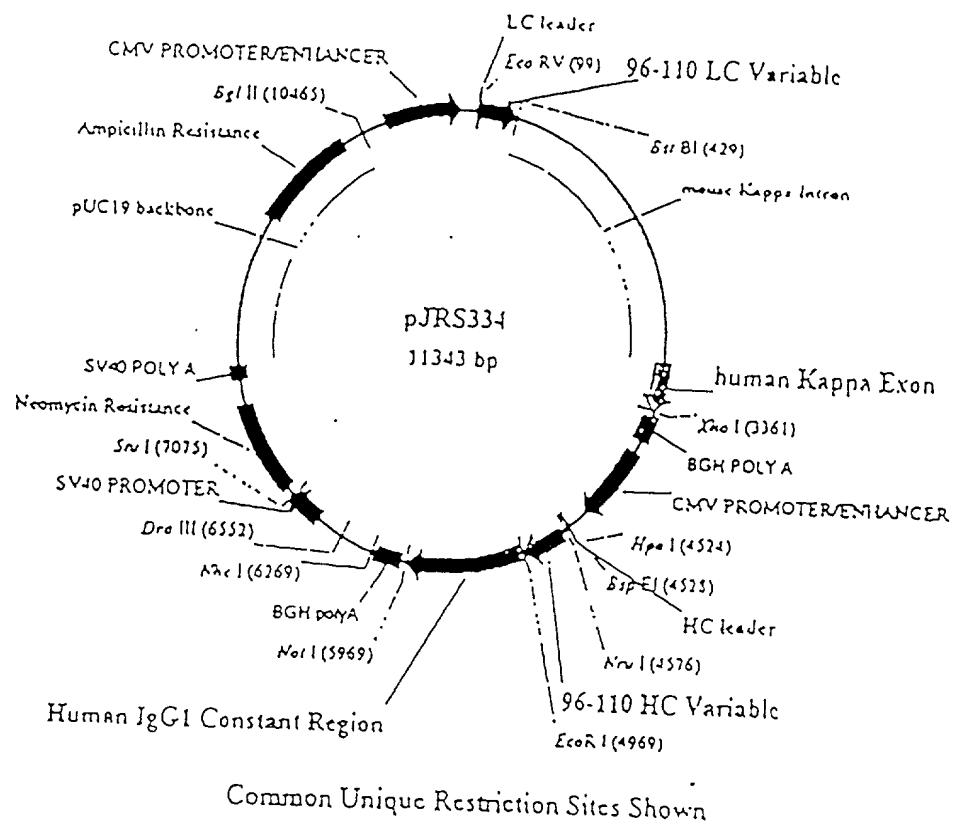


FIGURE 15: Antibody Production ELISA

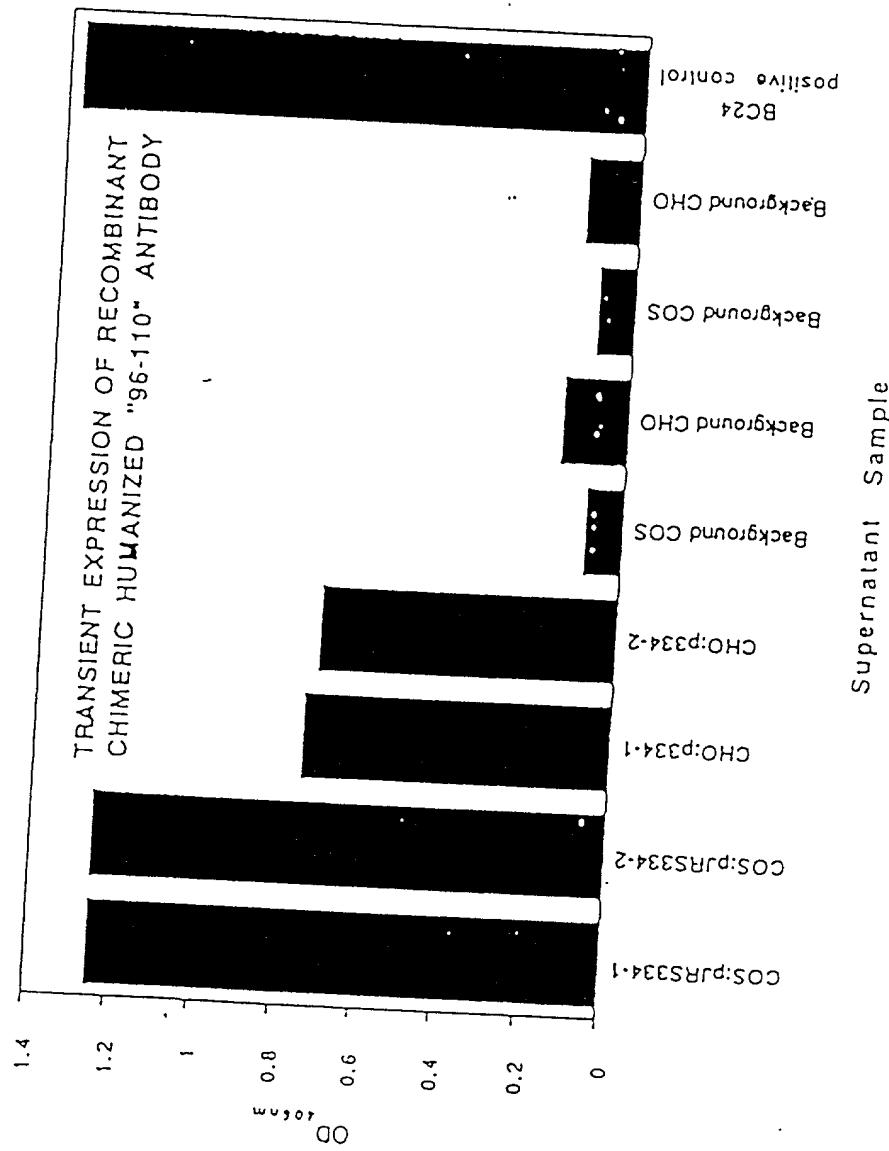
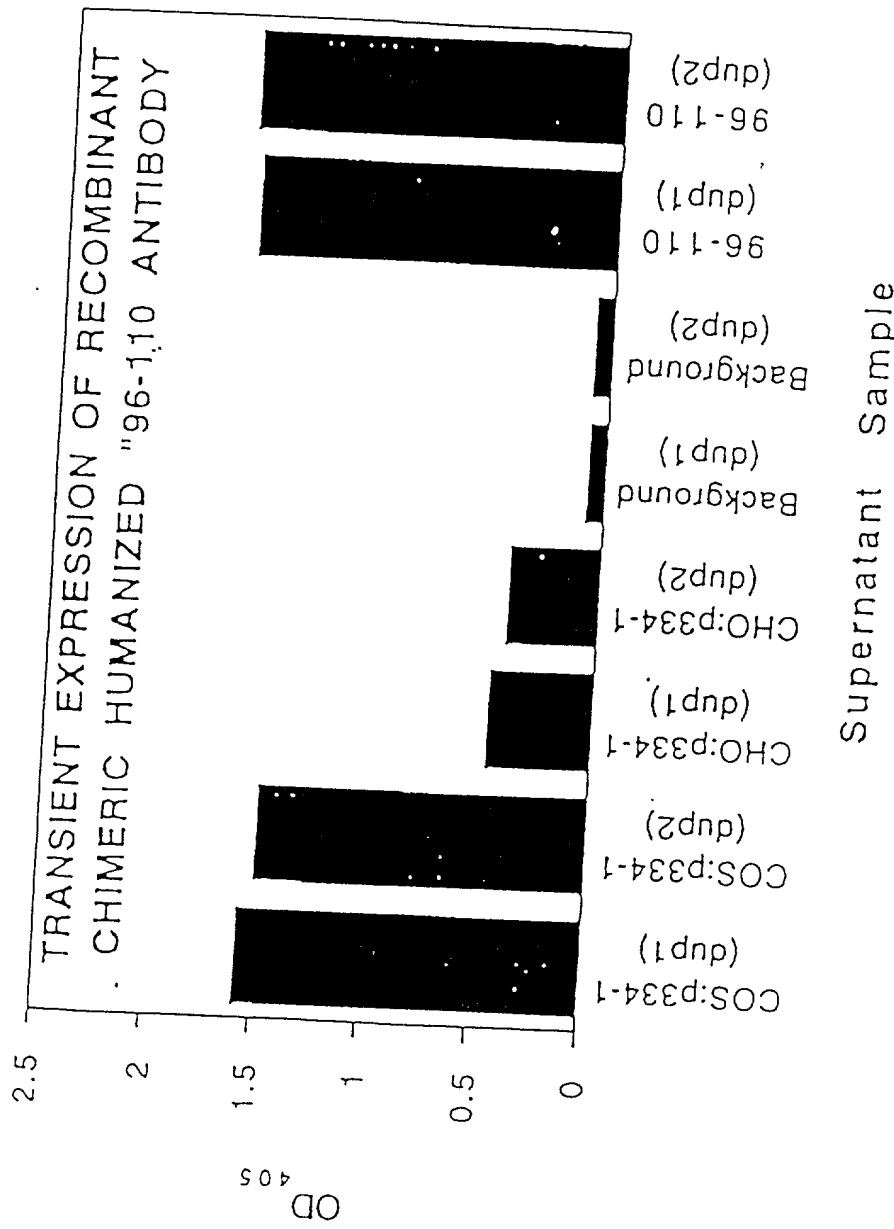
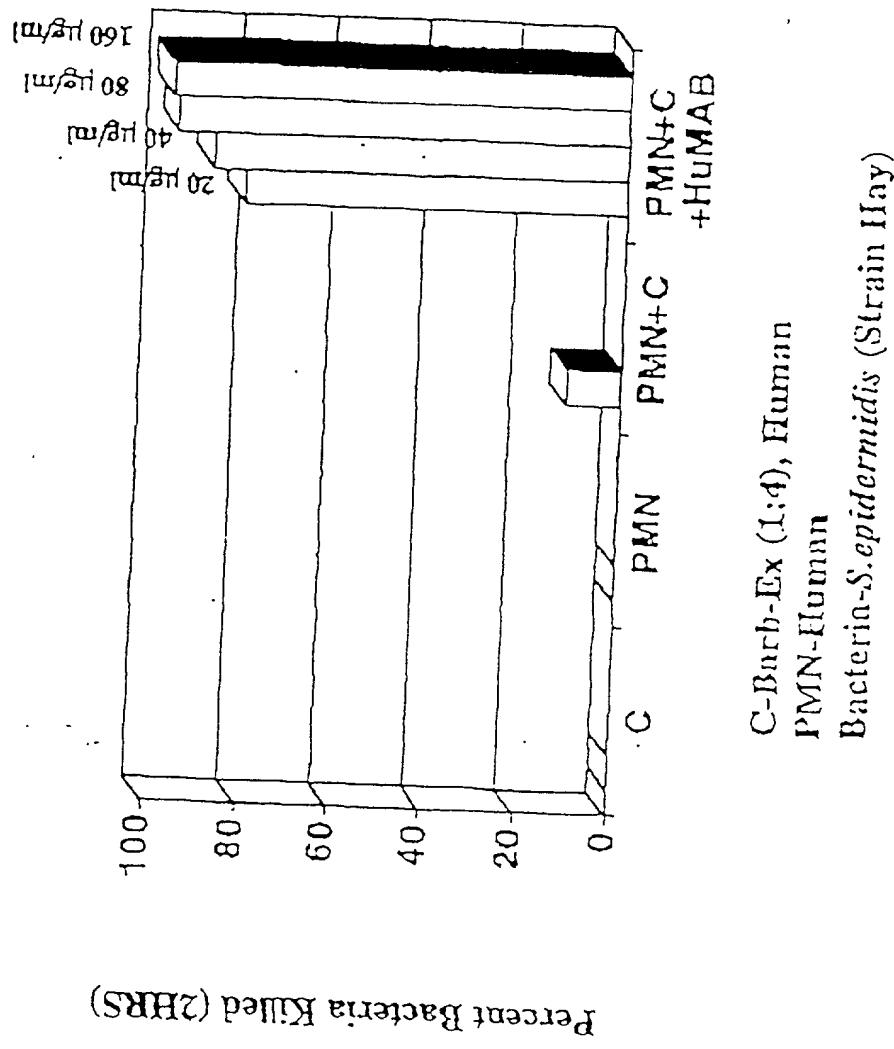


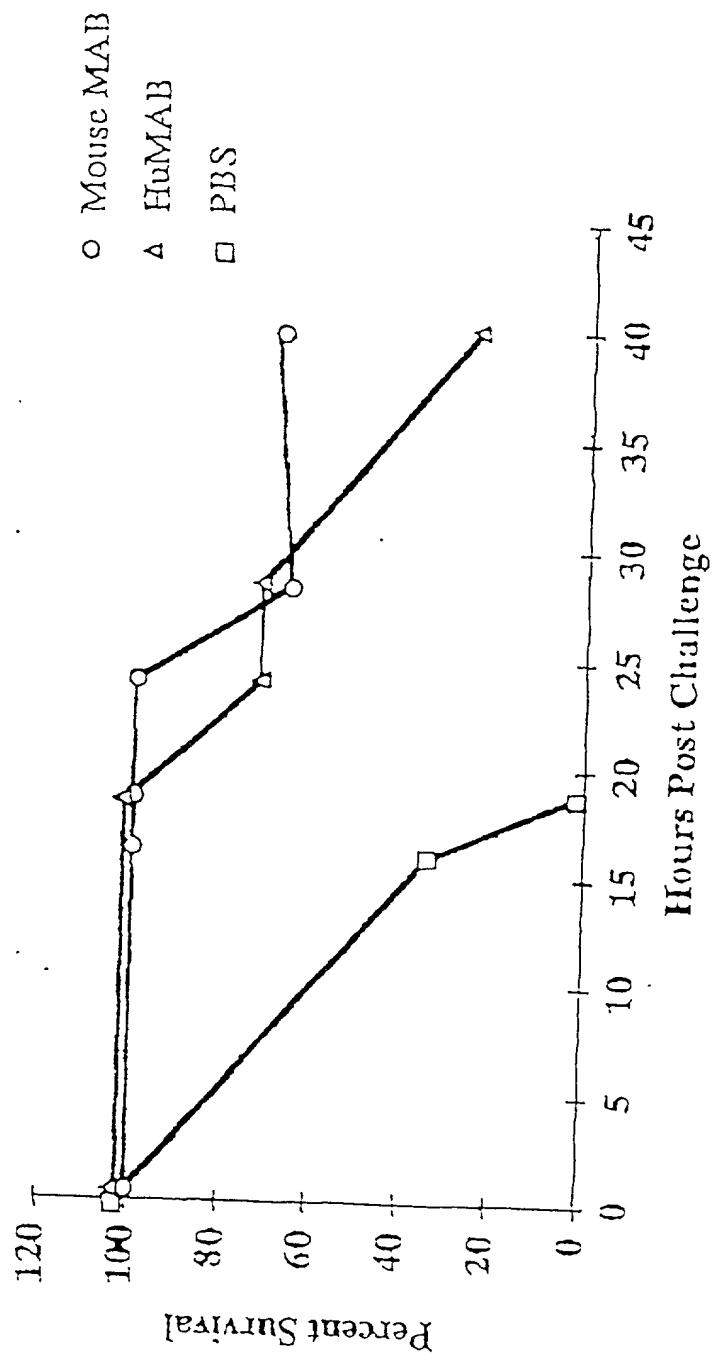
FIGURE 16: Anti-Staph HAY Activity ELISA



Opsonic Activity of HuMAB 96-110 for *S. epidermidis* in a Neutrophil Mediated Opsonophagocytic Bactericidal Assay Using Human Complement

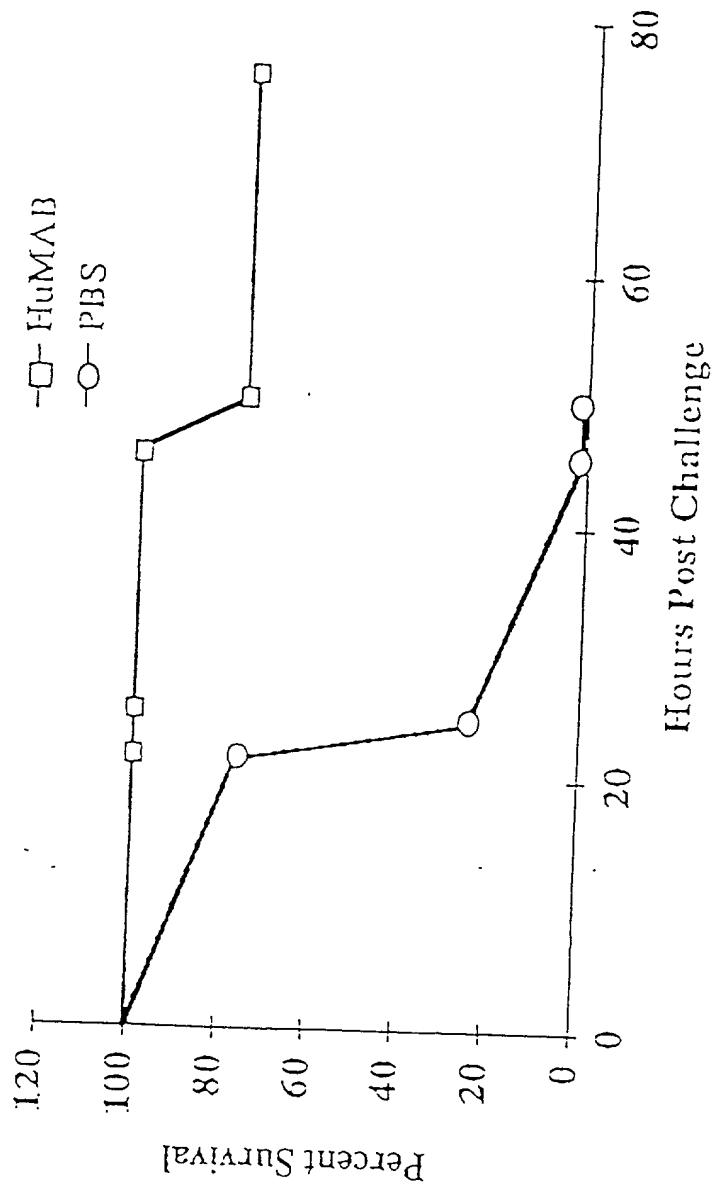


Pilot Study to Compare the Effect of Mouse MAB 96-110 and HuMAB 96-110 in a Lethal Model of *S. Epidermidis* Sepsis



MAB dose: 14 mg/kg given IP, 24 and 1 hour prior to infection

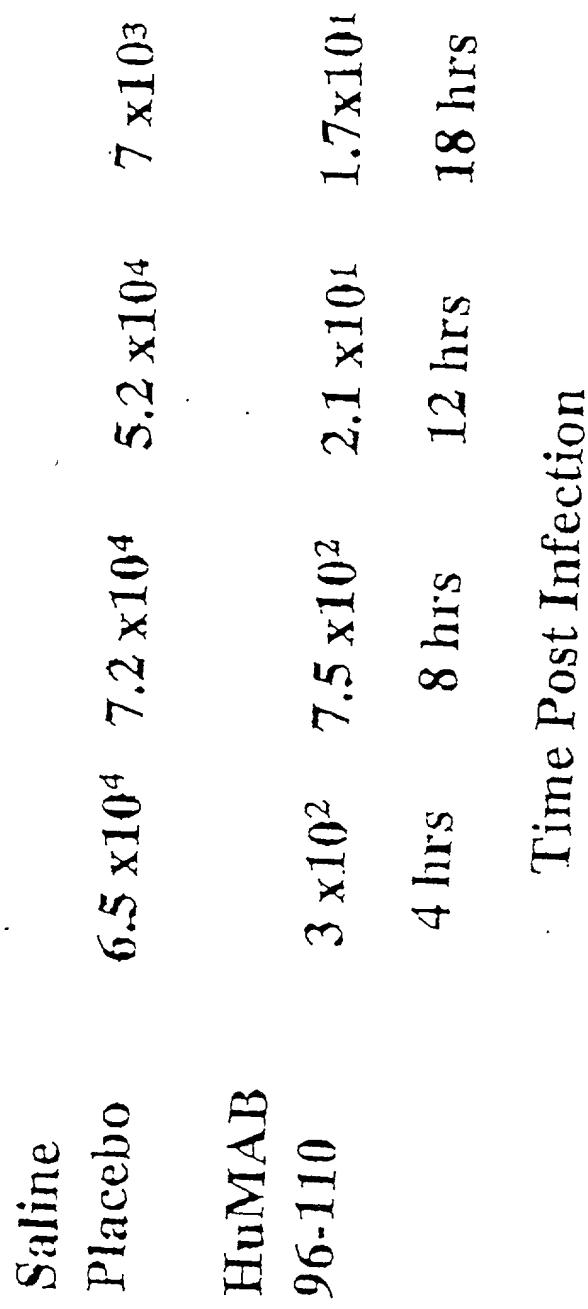
Survival of CF-1 Mice after Intraperitoneal Challenge with 3×10^9 *S. epidermidis* (Hay)



18 mg/kg/dose, IP, 24 and 1 hour prior to infection

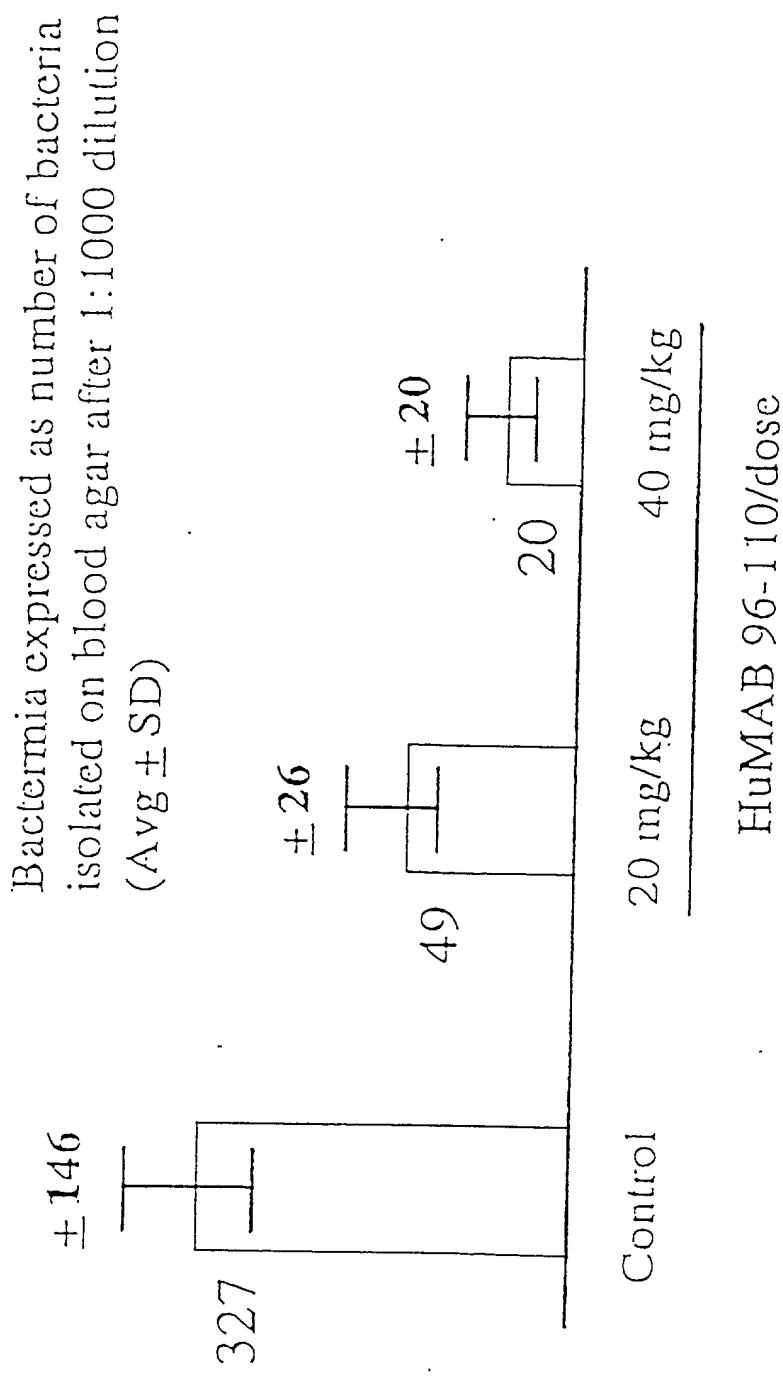
Effect of HuMAB 96-110 on Bacteremia in a Lethal *S. epidermidis* Sepsis Model

Geometric Mean Bacteremia Level



HuMAB 96-110 18 mg/kg/dose or saline given IP, 24 and 1 hour prior to IP infection with 3×10^9 *S. epidermidis* (HAY)

Bacteremia levels 4 hrs after infection with $3 \times 10^9 S. epidermidis$ *:



* CF-1 mice infected IP with strain Hay-HuMAB given IP x 2

The Effect of Hu 96-110 on Survival in a Lethal Neonatal *S. epidermidis** Sepsis Model: Study II

